

human EST clone 289913, GenBank Accession Number N71143
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/translation="GCAVAAALVLLGARAAGTSPRCDACGDFHKLGLFCGRG
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AVADTRCGKPGFVECVSSVPCPCDQCALHHRHLCSRRDTCGTCL
LGFEHGDGVCSPSTSLGSPERCAVGRWFQVQVLLAGLVPLLLGATLNTY
RHCWPKPLVTADEAGMALPPATHLSPDLSAHTLLAPDSSKICTVQLVNSWT
PCYPTQALCPQVNTDOLPSRALGPAAPATLSPSPAGSPAMMLQPGQLVDMD
APYARWFEVPTLGLREAEIIEAVEIGREFDQVEMLKRWRQOQAPGLGAVAALE
RMGLDGCEDLRSRQRP"
BASE COUNT 280 a 496 c 282 t
ORIGIN

Query Match 81.8%; Score 1511; DB 22; Length 1528;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 1515; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 252 GGGGCTGCGCGGGTGGCGGCGCTCCTCTGTGTGTGTGTGGGGGCGCGGCCAGG 311
Db 61 GCGGCACTCTAGCCCCAGTGTGACTGTGCCGTGACTTCCACAAAGATGGTCTGT 120
QY 312 GCGGCACTCTAGCCCCAGTGTGACTGTGCCGTGACTTCCACAAAGATGGTCTGT 371
Db 121 TTGTTTGCAGAGGCTGCCAGCGGGGACCTACCTGAAGGCCCTTGCACGAGCCCTGCG 180
QY 372 TTGTTTGCAGAGGCTGCCAGCGGGGACCTACCTGAAGGCCCTTGCACGAGCCCTGCG 431
Db 181 GCAACTCCACTGCTTGTGTGCCCAAGACACCTTCTTGGGCTGGGAGAACCCATTA 240
QY 432 GCAACTCCACTGCTTGTGTGCCCAAGACACCTTCTTGGGCTGGGAGAACCCATTA 491
Db 241 ATTCTGAATGTCGCGCTGCAGCGCTGTGATGAGAGGCTCCAGGTGGCGCTGGAGA 300
QY 492 ATTCTGAATGTCGCGCTGCAGCGCTGTGATGAGAGGCTCCAGGTGGCGCTGGAGA 551
Db 301 ACTGTTCCAGAGTGGCGGACACCGCTGTGGCTGTAAAGCCAGGCTGTGTTGTGAGTGC 360
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QY 612 AGGTACGCCAATGTGTCAGAGTTCACCTTCTACTGCCAACCATGCTAGACTGCGGG 671
Db 421 CCCTGACCGCCACACAGCGCTACTCTGTTCCCGCAGAGATAGTGTGGGACCTGCC 480
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QY 1032 ACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGTAAACAGCTGGACCCCTGGCTACC 1091
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QY 1692 AGACATTTCTCACTTCTCGCGCGGAGTTTGGCTGAGATGCGGGTATTAAATCTGTGAAA 1751
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QY 1752 GAAACAAACAAACAAACAA 1770

3
RESULT HS075380 1557 bp mRNA PRI 05-APR-1997
LOCUS Human apoptosis-mediating receptor TRAMP mRNA, partial cds.
DEFINITION U75380
ACCESSION
NID g1695924
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
REFERENCE 1 (bases 1 to 1557)
AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bolland, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,
French, L.E., Browning, J.L., MacDonald, R. and Tschopp, J.
TITLE TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)
JOURNAL Immunity 6 (1), 79-88 (1997)
MEDLINE 97205335
REFERENCE 2 (bases 1 to 1557)
AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bolland, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,

| 4 | RESULT | LOCUS | 1569 bp | mrna | PRI | 28-JAN-1998 |
|---|------------|--|---------|------|-----|-------------|
| | DEFINITION | Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds. | | | | |
| | ACCESSION | AF026070 | | | | |
| | VERSION | AF026070.1 | | | | |
| | KEYWORDS | NR_025708.3 | | | | |
| | SOURCE | human. | | | | |

4
RESULT
LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE

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US-08-943-776-1.rng

Fri Jul 17 07:49:29 1998

/note= "Max-interacting protein-2"

FT W09417101-A.
 PN 04-AUG-1994.
 PD 29-DEC-1993; U12643.
 PF 29-JAN-1993; US-011398.
 PR (GEO) GEN HOSPITAL-CORP.
 PA Brent R, Zervos AS;
 PI WPI: 94-264033/32.
 DR P-PSDB; R56543.
 DT Max-interacting polypeptide and DNA encoding them - used as
 PT anticancer agents and to screen for agents which inhibit cellular
 PT proliferation
 PS Disclosure: Page 41; 57pp; English.
 CC The DNA encodes Max-interacting (Mxi) protein-2. Detection of Mxi
 CC gene expression can be used to detect malignant cells in biological
 CC samples. The Mxi protein-2 and sense/antisense RNA can be delivered
 CC to e.g. bone marrow as therapeutic agents for cancer. 299 T;
 SQ Sequence 1200 BP; 306 A; 270 C; 325 G; 299 T;
 Length 1200;

Query Match 4.18; Score 75; DB 12; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 17 actcactataggcggaattgggtaccggcccccctcgaggtcgaggtatcgataagc 76
 Cp 1847 ACTCATTATAGGGCGAATTGGGTACCGGGCCCCCTCGAGGTGCGAGGTATCGATAAGC 1788
 Db 77 ttgatatcggaattcc 91
 Cp 1787 TTGATATCGAATTCC 1773

RESULT 8
 ID T91037 standard; cDNA to mRNA; 2150 BP.
 AC T91037;
 DT 25-FEB-1998 (first entry)
 DE Yeast checkpoint control gene RAD17 cDNA.
 KW Cancer; therapy: ss.
 OS Saccharomyces cerevisiae.
 FH Key Location/Qualifiers
 FT Key 741..1946
 FT CDS /*tag= a
 PN US5674996-A.
 PD 07-OCT-1997.
 PF 12-MAY-1992; 882051.
 PR 18-FEB-1994; US-198446.
 PR 12-MAY-1992; US-882051.
 PR 14-MAY-1992; US-884426.
 PR 12-MAY-1993; WO-U04458.
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PA (UNIV) UNIV ARIZONA.
 PA (UNIV) UNIV WASHINGTON.
 PI Groudine MT, Hartwell LH, Plon SE, Weinert TA;
 PI WPI: 97-502392/46.
 DR P-PSDB; W26661.
 DT Human cDNA sequence capable of hybridising with huCDC34 - which is
 PT human checkpoint gene, useful to increase sensitivity of tumour
 PT cells to chemotherapeutic drugs or radiation
 PS Example 4; Column 41-46; 54pp; English.
 CC Novel yeast checkpoint control genes RAD17, RAD24, MEC1, MEC2 and
 CC MEC3 (see T91037-41, respectively) are responsible for recognising
 CC if the cell has suffered DNA damage in the form of radiation or
 CC chemical damage or if the cell has failed to complete DNA
 CC replication because of chemical inhibition or intrinsic error.
 CC Upon recognising damage or failure, the genes are responsible
 CC for inhibiting mitosis. The purpose of this checkpoint control
 CC is that it preserves the viability of the cell and the integrity
 CC of the genome by providing the cell time to repair these insults
 CC prior to undertaking mitosis. The genes are potentially useful in
 CC developing cancer chemotherapeutics, cancer chemoprevention
 CC agents and environmental toxicology tests. They can be used to
 CC screen for

chemical agents that would interfere with checkpoint controls.
 CC Cloned genes can also be used to develop yeast strains in which to
 CC these genes are deleted. Such yeast strains can then be used to
 CC find the homologous human genes (see T91034-36).
 CC Sequence 2150 BP; 748 A; 372 C; 425 G; 605 T;
 SQ

Query Match 4.18; Score 75; DB 35; Length 2150;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 actcactataggcggaattgggtaccggcccccctcgaggtcgaggtatcgataagc 128
 Cp 1847 ACTCATTATAGGGCGAATTGGGTACCGGGCCCCCTCGAGGTGCGAGGTATCGATAAGC 1788
 Db 129 ttgatatcggaattcc 143
 Cp 1787 TTGATATCGAATTCC 1773

RESULT 9
 ID Q48463 standard; DNA; 3792 BP.
 AC Q48463;
 DT 18-MAR-1994 (first entry)
 DE Plasmid pG+host4 containing Ts replication system.
 KW Temperature sensitive replication; antibiotic resistance marker gene;
 KW site-specific recombination; chromosomal integration; inactivation;
 KW heterologous gene expression; thermosensitive plasmid; ds.
 OS Synthetic.
 PN WO9318164-A.
 PD 16-SEP-1993.
 PF 12-MAR-1993; F00248.
 PR 13-MAR-1992; FR-003034.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PI Gruss A, Maguin E;
 PI WPI: 93-303478/38.
 DT New bacterial plasmid contg. heat sensitive replication system -
 PT and marker gene, opt. capable of chromosomal integration, used to
 PT inactivate specific gene or introduce heterologous gene
 PS Example 2; Fig 9; 73pp; French.
 CC Plasmid pGK12 (Appl. Environ. Microbiol., 48; 726 (1984)) contg. two
 CC antibiotic resistance marker genes was subjected to mutagenesis with
 CC hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
 CC sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and
 CC the 340bp fragment lacking the Cm resistance gene was ligated to a
 CC 445bp PvuII fragment of pBluescript SK+ containing a multicloning
 CC site, T7 and T3 promoters and sequencing primer binding sites. The
 CC resulting plasmid was designated pVE5004 (or pG+host4 - Q48463). It
 CC is thermosensitive in all hosts tested, including E.coli, and must be
 CC maintained at 28 deg.C.
 SQ Sequence 3792 BP; 1249 A; 552 C; 742 G; 1249 T;

Query Match 4.18; Score 75; DB 8; Length 3792;
 Best Local Similarity 100.0%; Pred. No. 1.73e-24;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3448 actcactataggcggaattgggtaccggcccccctcgaggtcgaggtatcgataagc 3507
 Cp 1847 ACTCATTATAGGGCGAATTGGGTACCGGGCCCCCTCGAGGTGCGAGGTATCGATAAGC 1788
 Db 3508 ttgatatcggaattcc 3522
 Cp 1787 TTGATATCGAATTCC 1773

RESULT 10
 ID Q48464 standard; DNA; 5234 BP.
 AC Q48464;
 DT 18-MAR-1994 (first entry)
 DE Plasmid pG+host5 containing Ts replication system.
 KW Temperature sensitive replication; antibiotic resistance marker gene;
 KW site-specific recombination; chromosomal integration; inactivation;
 KW heterologous gene expression; thermosensitive plasmid; ds.
 OS Synthetic.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 19, 2001, 15:26:43 ; Search time 50.46 Seconds
(without alignments)
148.397 Million cell updates/sec

Title: US-08-943-776-2

Perfect score: 2323

Sequence: 1 MEQPRGCAAAVALLVLL.....ERMGLDGVCLRLRQGP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgnl_7/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgnl_7/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgnl_7/ptodata/1/iaa/6.COMB.pep.*
- 4: /cgnl_7/ptodata/1/iaa/PTCUS.COMB.pep.*
- 5: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 2323 | 100.0 | 417 | 3 | US-08-815-469-4 |
| 2 | 2267 | 97.6 | 428 | 3 | US-08-815-469-2 |
| 3 | 376 | 16.2 | 455 | 1 | US-08-050-319B-25 |
| 4 | 376 | 16.2 | 455 | 2 | US-08-465-982-25 |
| 5 | 374 | 16.1 | 455 | 1 | US-08-321-668-2 |
| 6 | 374 | 16.1 | 455 | 1 | US-08-837-941-2 |
| 7 | 374 | 16.1 | 455 | 2 | US-08-126-016-2 |
| 8 | 374 | 16.1 | 455 | 3 | US-08-815-469-5 |
| 9 | 217 | 9.3 | 280 | 3 | US-08-974-022-46 |
| 10 | 210 | 9.0 | 199 | 1 | US-08-050-319B-48 |
| 11 | 210 | 9.0 | 199 | 2 | US-08-465-982-48 |
| 12 | 207.5 | 8.9 | 283 | 4 | PCT-US96-12374-2 |
| 13 | 203.5 | 8.8 | 440 | 3 | US-08-883-036A-2 |
| 14 | 200.5 | 8.6 | 153 | 2 | US-08-219-237B-4 |
| 15 | 199.5 | 8.6 | 335 | 2 | US-08-219-237B-2 |
| 16 | 199.5 | 8.6 | 335 | 2 | US-08-409-338-1 |
| 17 | 199.5 | 8.6 | 335 | 4 | PCT-US95-17083-2 |
| 18 | 198.5 | 8.5 | 154 | 2 | US-08-232-087A-10 |
| 19 | 197.5 | 8.5 | 335 | 3 | US-08-815-469-6 |
| 20 | 189.5 | 8.2 | 368 | 2 | US-08-651-579-2 |
| 21 | 176.5 | 7.6 | 219 | 3 | US-08-974-022-45 |
| 22 | 175.5 | 7.6 | 158 | 1 | US-08-050-319B-54 |
| 23 | 175.5 | 7.6 | 158 | 2 | US-08-465-982-54 |
| 24 | 168 | 7.2 | 314 | 1 | US-08-444-231-19 |
| 25 | 168 | 7.2 | 314 | 1 | US-08-152-443A-19 |
| 26 | 168 | 7.2 | 314 | 4 | PCT-US95-17083-4 |
| 27 | 166 | 7.1 | 167 | 1 | US-08-050-319B-2 |
| 28 | 166 | 7.1 | 167 | 1 | US-08-050-319B-57 |

Sequence 2, Appl
Sequence 57, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 2, Appl
Sequence 20, Appl
Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-4
; Sequence 4, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-815-469-4

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Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDQASQVALENCSSAVADTRCGCKPG 120
QY 121 WVEVCQVSCQVSSSPFFCQPCDCLGALHRTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
Db 121 WVEVCQVSCQVSSSPFFCQPCDCLGALHRTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
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Db 181 TSTIGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTTRHCHWPKPLVTADEAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSTPGYPTQALCPQVTVSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSTPGYPTQALCPQVTVSW 300
QY 301 DOLPSRAGPAAAPTILSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DOLPSRAGPAAAPTILSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFDQOQYEMLKRWRQOPAGLGVAYTAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKRWRQOPAGLGVAYTAALERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-08-943-776-2
Sequence 2, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
AGENT INFORMATION:

NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-469-2

Query Match 97.6%; Score 2367; DB 3; Length 428;
Best Local Similarity 97.1%; Pred. No. 7.5e-189;
Matches 409; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 3 QPRG-----CAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHY 56
Db 8 EAPRGQLRGESAAVPVQALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHY 67
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Db 57 LKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARQACDQASQVALENCSSAVADTRCG 127
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Db 128 CKPGWFVEVCQVSCQVSSSPFFCQPCDCLGALHRTLLCSRRDTCGTCPLPGFYEHDGDC 187
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Db 248 DEAGNEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSTPGYPTQALCPQV 307
QY 297 TWSWDQLPSRALGPAAPTILSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGL 356
Db 308 TWSWDQLPSRALGPAAPTILSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGL 367
QY 357 REABIEAVEVEIGRFDQOQYEMLKRWRQOPAGLGVAYTAALERMGLDGCVEDLRSRLQ 416
Db 368 REABIEAVEVEIGRFDQOQYEMLKRWRQOPAGLGVAYTAALERMGLDGCVEDLRSRLQ 427
QY 417 P 417
Db 428 P 428

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 10:49:23 ; Search time 65.08 Seconds
(without alignments)
4573.803 Million cell updates/sec

Title: US-08-943-776-1
Perfect score: 1847
Sequence: 1 CTTTCACCCATACCCGGAT.....CAATTCGCCCTACTAGT 1847

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq: *
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq: *
3: /cgnl_7/ptodata/1/ina/6_COMB.seq: *
4: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq: *
5: /cgnl_7/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 1495 | 80.9 | 1783 | 3 | US-08-815-469-1 |
| 2 | 1254 | 67.9 | 1254 | 3 | US-08-815-469-3 |
| 3 | 172 | 9.3 | 1858 | 2 | US-08-909-965C-11 |
| 4 | 75.4 | 4.1 | 1023 | 1 | US-08-198-446B-1 |
| 5 | 75.4 | 4.1 | 1023 | 2 | US-08-870-693-1 |
| 6 | 75.4 | 4.1 | 1200 | 1 | US-08-011-398B-3 |
| 7 | 75.4 | 4.1 | 1200 | 1 | US-08-464-051-3 |
| 8 | 75.4 | 4.1 | 1200 | 2 | US-08-462-498-3 |
| 9 | 75.4 | 4.1 | 2150 | 1 | US-08-198-446B-10 |
| 10 | 75.4 | 4.1 | 2150 | 2 | US-08-870-693-10 |
| 11 | 75.4 | 4.1 | 3792 | 3 | US-08-992-334-1 |
| 12 | 75.4 | 4.1 | 3792 | 3 | US-08-302-752-1 |
| 13 | 75.4 | 4.1 | 5234 | 2 | US-08-992-334-2 |
| 14 | 75.4 | 4.1 | 5234 | 3 | US-08-302-752-2 |
| 15 | 75.4 | 4.1 | 6722 | 2 | US-08-992-334-3 |
| 16 | 75.4 | 4.1 | 6722 | 3 | US-08-302-752-3 |
| 17 | 74.4 | 4.0 | 2605 | 2 | US-08-680-395-4 |
| 18 | 74.2 | 4.0 | 5534 | 1 | US-08-452-267-3 |
| 19 | 74.2 | 4.0 | 5534 | 3 | US-09-123-644-3 |
| 20 | 70.6 | 3.8 | 2161 | 3 | US-09-106-038A-1 |
| 21 | 70.6 | 3.8 | 2175 | 1 | US-08-321-668-1 |
| 22 | 70.6 | 3.8 | 2175 | 1 | US-08-837-941-1 |
| 23 | 70.6 | 3.8 | 2175 | 1 | US-08-126-016-1 |
| 24 | 69 | 3.7 | 2062 | 1 | US-08-050-319B-24 |
| 25 | 69 | 3.7 | 2062 | 2 | US-08-463-982-24 |
| 26 | 68.8 | 3.7 | 685 | 1 | US-08-463-115-56 |
| 27 | 68.8 | 3.7 | 685 | 1 | US-08-465-388-56 |
| 28 | 67 | 3.6 | 405 | 2 | US-08-299-074A-1 |

Sequence 2, Appli
Sequence 6, Appli
Sequence 22, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 113, App
Sequence 113, App
Sequence 113, App
Sequence 10, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 1, Appli
Sequence 59, Appl

29 67 3.6 4525 2 US-08-613-861-2
30 65 3.5 3699 3 US-08-646-538-6
31 65 3.5 4965 3 US-08-675-566-22
32 62 3.4 6994 3 US-08-675-566-1
33 62 3.4 7001 3 US-08-675-566-3
34 60.4 3.3 2185 2 US-08-467-948A-3
35 60.4 3.3 2185 3 US-08-467-947A-3
36 59 3.2 834 2 US-08-967-101-113
37 59 3.2 834 2 US-08-592-541-113
38 59 3.2 834 3 US-09-124-698-113
39 58.8 3.2 1956 2 US-08-762-308-10
40 58.6 3.2 141 2 US-08-454-557C-83
41 58.6 3.2 141 2 US-08-340-426D-83
42 58.6 3.2 141 2 US-08-450-673C-83
43 58.6 3.2 141 4 PCT-US95-17111A-83
44 57.6 3.1 2764 2 US-08-465-971B-1
45 57.6 3.1 3560 3 US-08-833-391-59

ALIGNMENTS

RESULT 1
US-08-815-469-1
; Sequence 1, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA


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FEATURE:
; NAME/KEY: CDS
; LOCATION: 198..1481
; US-08-815-469-1

Query Match      80.9%; Score 1495; DB 3; Length 1783;
Best Local Similarity 99.3%; Pred. No. 1.3e-299;
Matches 1501; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 260 GCGCGGTGGCGCGCGCTCTCCCTGGTGTGCTGGGGGCGCGCGCCAGCGCGGCACT 319
DB 255 GCACCTGTCCCGCAGCGCTCTCTCTGGTGTGCTGGGGGCGCGCGCCAGCGGCGCACT 314
QY 320 CGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCACAGAAGATTGGTCTGTTTGTTCG 379
DB 315 CGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCACAGAAGATTGGTCTGTTTGTTCG 374
QY 380 AGAGGTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGGCCCTGCGGCACTCC 439
DB 375 AGAGGTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGGCCCTGCGGCACTCC 434
QY 440 ACTCGCTTGTGTGTCGCCAAGACACTTCTTGGCTGGGAGAACACCATATCTGAA 499
DB 435 ACTCGCTTGTGTGTCGCCAAGACACTTCTTGGCTGGGAGAACACCATATCTGAA 494
QY 500 TGTGCGCGTGCACAGCCCTGTGATGAGCAGGCTTCCAGGTGGCGTGGAGAACTGTTC 559
DB 495 TGTGCGCGTGCACAGCCCTGTGATGAGCAGGCTTCCAGGTGGCGTGGAGAACTGTTC 554
QY 560 GCAGTGGCGGACACCGCGTGTGCTGTAGCAGGCTGTGTTGTGAGTGCAGGTGACG 619
DB 555 GCAGTGGCGGACACCGCGTGTGCTGTAGCAGGCTGTGTTGTGAGTGCAGGTGACG 614
QY 620 CAATGTGTGAGCAGTTACCCCTTCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCAC 679
DB 615 CAATGTGTGAGCAGTTACCCCTTCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCAC 674
QY 680 CGCCACACACGGCTACTCTGTGCCGAGAGATACACTGTGGGACCTGCTGCTGGC 739
DB 675 CGCCACACACGGCTACTCTGTGCCGAGAGATACACTGTGGGACCTGCTGCTGGC 734
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DB 735 TTCTATGACATGGCGATGGCTGCTGTGCTGCCGCCAGCAGCACCTGGGAGCTGTCCA 794
QY 800 GAGCGCTGTGCGCTCTCTGTGCTGGAGGAGATGCTTCTGGGTCCAGTGTCTGGCT 859
DB 795 GAGCGCTGTGCGCTCTCTGTGCTGGAGGAGATGCTTCTGGGTCCAGTGTCTGGCT 854
QY 860 GGCTTGTGTGCTCCCTCTCTGCTTGGGGCCACCTGACCTACACATACCGCCACTGCTGG 919
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DB 915 CCTCACAAGCCCTGCTTACTGCAGATGAAGCTGGGATGAGGCTCTGACCCACCAACCG 974
QY 980 GCCACCCATCTGACCCCTTGGACGCGGCCACACCCCTCTAGCACTCTCTGACAGCACT 1039
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QY 1040 GAGAAGATCTGACCCCTTCCAGTTGGTGGTAAACAGCTGGACCCCTGGCTACCCGAGACC 1099
DB 1035 GAGAAGATCTGACCCCTTCCAGTTGGTGGTAAACAGCTGGACCCCTGGCTACCCGAGACC 1094
QY 1100 CAGGAGCGCTCTGCCCGCAGGTGACATGGTCTCTGGGACCACTTGGCCACGAGAGCTT 1159
DB 1095 CAGGAGCGCTCTGCCCGCAGGTGACATGGTCTCTGGGACCACTTGGCCACGAGAGCTT 1154
QY 1160 GGCCCGCTGCTGCGGCCACACTCTCTCGCAGAGTCCCGCAGCGGCTGCGCCAGCATGATG 1219
DB 1155 GCGCGCTGCTGCGGCCACACTCTCTCGCAGAGTCCCGCAGCGGCTGCGCCAGCATGATG 1214

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Query Match 67.9%; Score 1254; DB 3; Length 1254;
Best Local Similarity 100.0%; Pred. No. 5e-250;
Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 236 | ATGGAGACGCGCGCGGCTGCGCGGCTGGCGGCGGCGCTCCTCTGCTGCTGCTG | 295 |
| DB | 1 | ATGGAGACGCGCGCGGCTGCGCGGCTGGCGGCGGCGCTCCTCTGCTGCTGCTG | 60 |
| QY | 296 | GGGGCCCGGGCCAGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCAC | 355 |
| DB | 61 | GGGGCCCGGGCCAGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCAC | 120 |
| QY | 356 | AGAGAGATGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGCCCT | 415 |
| DB | 121 | AGAGAGATGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGCCCT | 180 |
| QY | 416 | TGCAGGAGCCCTGGCGCACTCCACCTGCCTGTGTGTGCCCAAGACACCTTCTTGGCC | 475 |
| DB | 181 | TGCAGGAGCCCTGGCGCACTCCACCTGCCTGTGTGTGCCCAAGACACCTTCTTGGCC | 240 |
| QY | 476 | TGGGAGAACCAACATAATTTCTGAATGTGCCCGTCCAGGCTGTGATGAGCAGGCTCC | 535 |
| DB | 241 | TGGGAGAACCAACATAATTTCTGAATGTGCCCGTCCAGGCTGTGATGAGCAGGCTCC | 300 |
| QY | 536 | CAGGTGGCGCTGGAGACTGTTTCCAGAGTGGCGACACCGCTGTGGCTGAAGCCAGGC | 595 |
| DB | 301 | CAGGTGGCGCTGGAGACTGTTTCCAGAGTGGCGACACCGCTGTGGCTGAAGCCAGGC | 360 |
| QY | 596 | TGTTTGTGGAGTGGCAGGTGAGCAATGTGTGAGAGTTCACCCCTTCTACTGCCAACCA | 655 |
| DB | 361 | TGTTTGTGGAGTGGCAGGTGAGCAATGTGTGAGAGTTCACCCCTTCTACTGCCAACCA | 420 |
| QY | 656 | TGCCTAGACTGGGGGCCCTGACCCGCCACACAGGCTACTCTGTTTCCCGCAGAGATACT | 715 |
| DB | 421 | TGCCTAGACTGGGGGCCCTGACCCGCCACACAGGCTACTCTGTTTCCCGCAGAGATACT | 480 |
| QY | 716 | GACTGTGGAGCTGCTGCTGCTGCTTCTATGAACTGGGAGTGGCTGTGCTGCTGCTG | 775 |
| DB | 481 | GACTGTGGAGCTGCTGCTGCTGCTTCTATGAACTGGGAGTGGCTGTGCTGCTGCTG | 540 |
| QY | 776 | ACGAGACACCTGGGAGCTGTCAGAGCGCTGTGCCGTGTCTGTGGCTGGAGGAGATG | 835 |
| DB | 541 | ACGAGACACCTGGGAGCTGTCAGAGCGCTGTGCCGTGTCTGTGGCTGGAGGAGATG | 600 |
| QY | 836 | TTCCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 895 |
| DB | 601 | TTCCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 660 |

| | | | |
|----|------|---|------|
| QY | 896 | ACCTACATACCGCCACTGCTGGCCTCAAGCCCTGTTACTGAGATGAGCTGGG | 955 |
| DB | 661 | ACCTACATACCGCCACTGCTGGCCTCAAGCCCTGTTACTGAGATGAGCTGGG | 720 |
| QY | 956 | ATGGAGCTGTGACCCACACCGGCGCCATCTGACCCCTTGGACGCGCCACACC | 1015 |
| DB | 721 | ATGGAGCTGTGACCCACACCGGCGCCATCTGACCCCTTGGACGCGCCACACC | 780 |
| QY | 1016 | CTTCTAGCACCTCTGACAGCAGTGAAGATCTGACCCCTTGGACGCGCCACACC | 1075 |
| DB | 781 | CTTCTAGCACCTCTGACAGCAGTGAAGATCTGACCCCTTGGACGCGCCACACC | 840 |
| QY | 1076 | TGGACCCCTGCTACCCCGGAGACCCAGAGGCGCTGTGCCCGCAGGTGATGCTGG | 1135 |
| DB | 841 | TGGACCCCTGCTACCCCGGAGACCCAGAGGCGCTGTGCCCGCAGGTGATGCTGG | 900 |
| QY | 1136 | GACAGTTGCCACGACAGAGCTTGGCCCGCTGCTGGCCCGCACACTCTGCCAGAGTCC | 1195 |
| DB | 901 | GACAGTTGCCACGACAGAGCTTGGCCCGCTGCTGGCCCGCACACTCTGCCAGAGTCC | 960 |
| QY | 1196 | CCAGCGGCTGCCAGCCATGATCTGCAGCGCGGCGCGCAGCTCTACGAGCTGATGAC | 1255 |
| DB | 961 | CCAGCGGCTGCCAGCCATGATCTGCAGCGCGGCGCGCAGCTCTACGAGCTGATGAC | 1020 |
| QY | 1256 | GCGGTCCCGCGCGGCTGGAAGAGTTGTCGCGCAGCTGGGCTGCGGAGGACAGAG | 1315 |
| DB | 1021 | GCGGTCCCGCGCGGCTGGAAGAGTTGTCGCGCAGCTGGGCTGCGGAGGACAGAG | 1080 |
| QY | 1316 | ATCGAAGCCGTGGAGGTGGAGATCGGCGCTTCCGAGACGAGTACGAGATGCTCAAG | 1375 |
| DB | 1081 | ATCGAAGCCGTGGAGGTGGAGATCGGCGCTTCCGAGACGAGTACGAGATGCTCAAG | 1140 |
| QY | 1376 | CGCTGGCGCAGCAGCAGCGCGGCTTACGCGGCTTACGCGGCTTGGAGCGCATG | 1435 |
| DB | 1141 | CGCTGGCGCAGCAGCAGCGCGGCTTACGCGGCTTACGCGGCTTGGAGCGCATG | 1200 |
| QY | 1436 | GGGCTGGAGCGCTGCGTGAAGACTTGCAGCGCGCTTGCAGCGCGGCGGCTGA | 1489 |
| DB | 1201 | GGGCTGGAGCGCTGCGTGAAGACTTGCAGCGCGCTTGCAGCGCGGCGGCTGA | 1254 |